

FIGURE 1

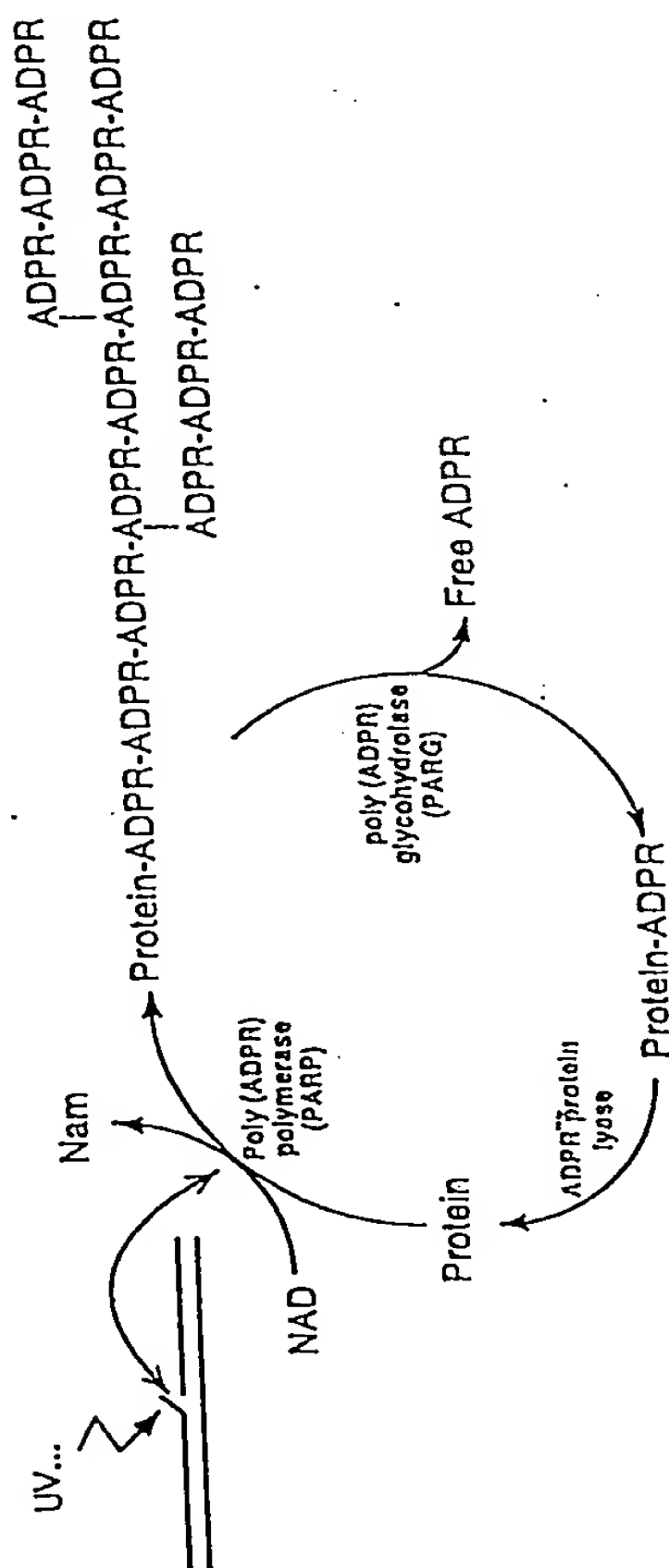
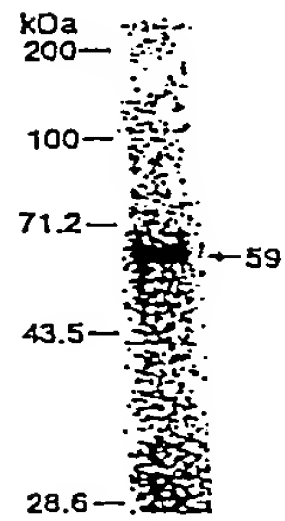


FIGURE 2



0947431 400901
T0600T T044E/060

FIGURE 3

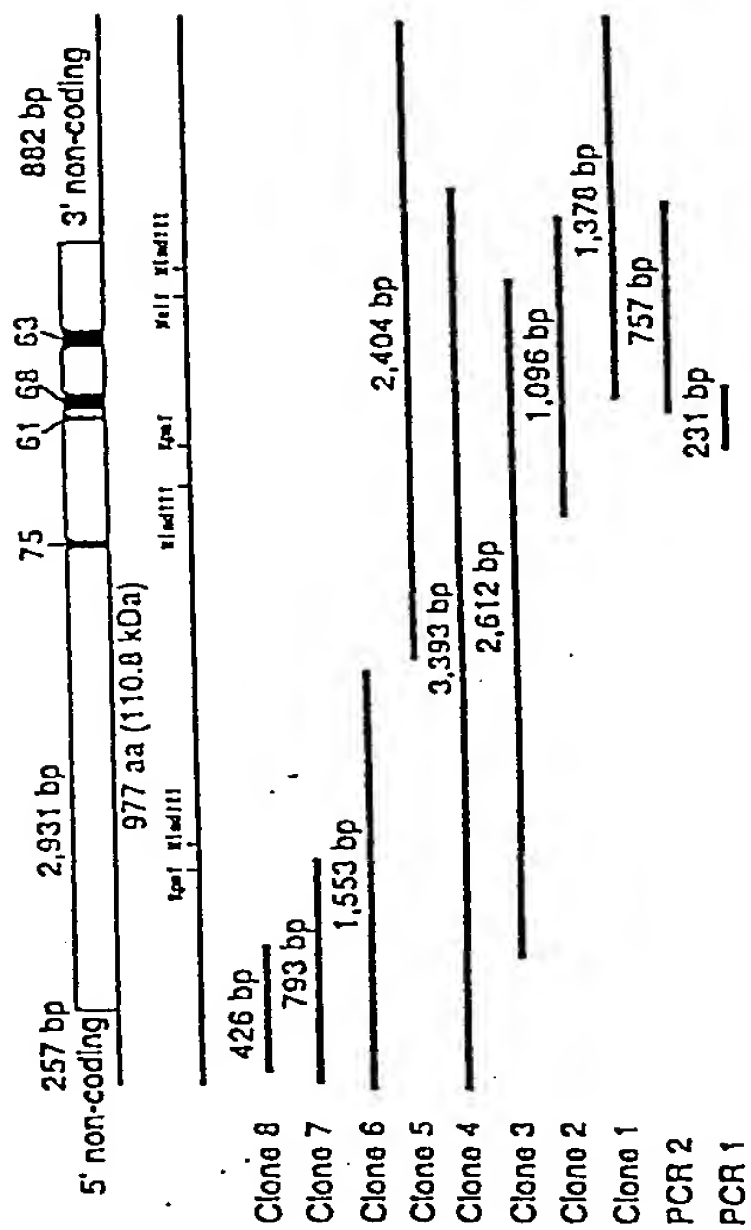
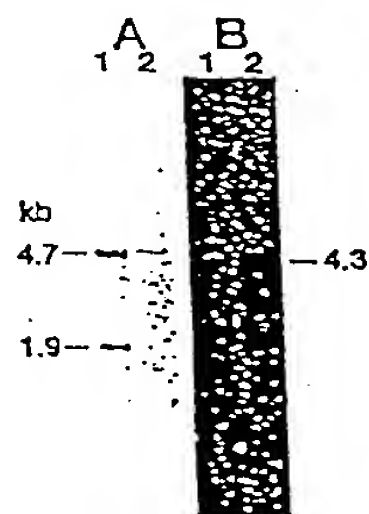


FIGURE 4



0697491-100501

FIGURE 5

bPARG	(422)	ED.....KRKEQCEMKHQ RTE..RKIPKYIPPH	SEQ ID NO: 19
hPARG	(421)	ED.....RRKEQWETKHQ RTE..RKIPKYVPPH	SEQ ID NO: 20
mPARG	(413)	ED.....RRKEQCEVRHQ RTE..RKIPKYIPPN	SEQ ID NO: 21
CePARG	(29)	HQVPTMKRRRLTEHGNTTESLLKEDPEEPKS	SEQ ID NO: 22
hPARG	(205)	EG.....KRKGD.EVDG.VDEVAKKSKKEKDK	SEQ ID NO: 23
mPARG	(205)	EG.....KRKGD.EVDG.TDEVAKKSKRKETDK	SEQ ID NO: 24
bPARG	(208)	EG.....KRKGD.EVDG.IDEVTKKKSKKEKDK	SEQ ID NO: 25
aPARG	(205)	EG.....KRKGE.EVDG..NVVAKKSKRKEKEK	SEQ ID NO: 26
XIPARG	(204)	EG.....KRKAD.EVDG.HSAATKKKIKKEKEK	SEQ ID NO: 27
DmPARG	(202)	EELPDTKRAKM.ELSDTNEEGEKKQR.....	SEQ ID NO: 28
SpPARG	(205)	EGVSSAKKAKI.EKIDEEAASIKELTEKIKK	SEQ ID NO: 29

SECRET

FIGURE 6

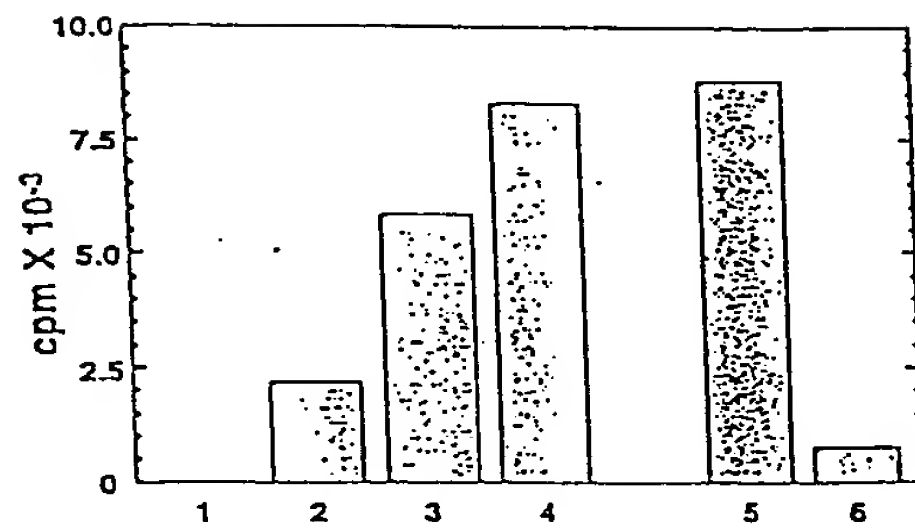
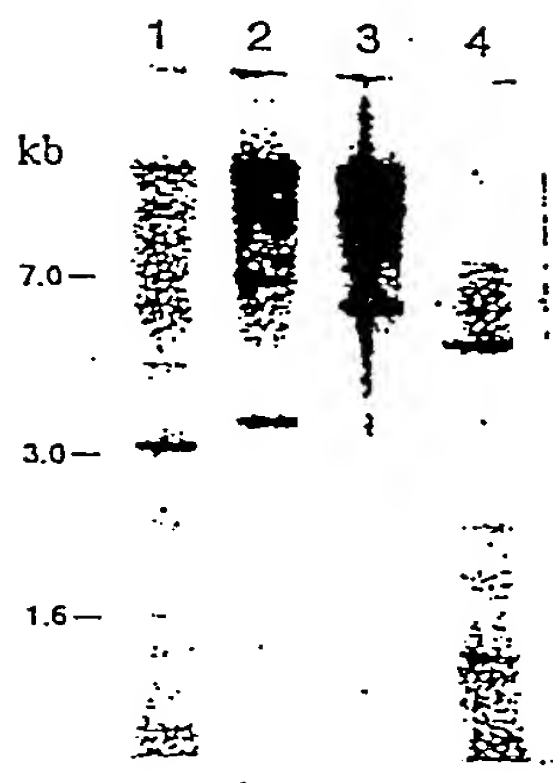
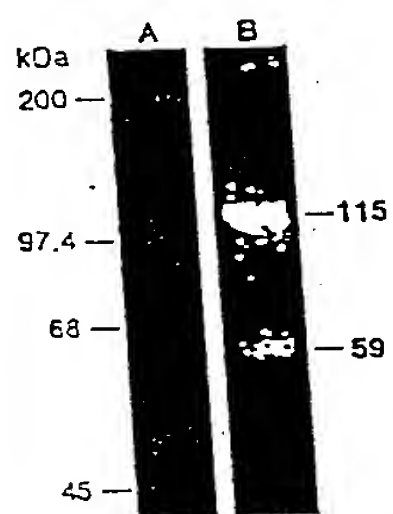


FIGURE 7



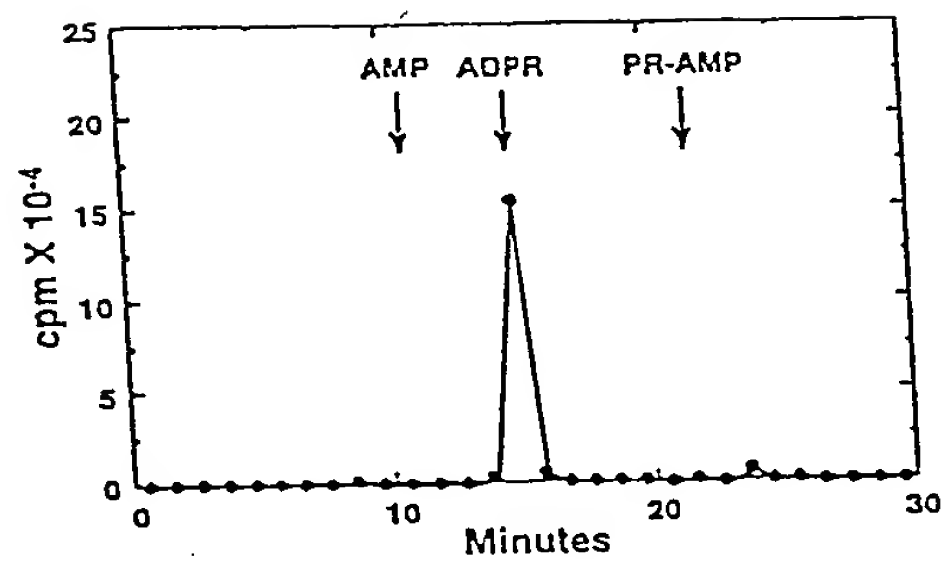
09572464.100901

FIGURE 8



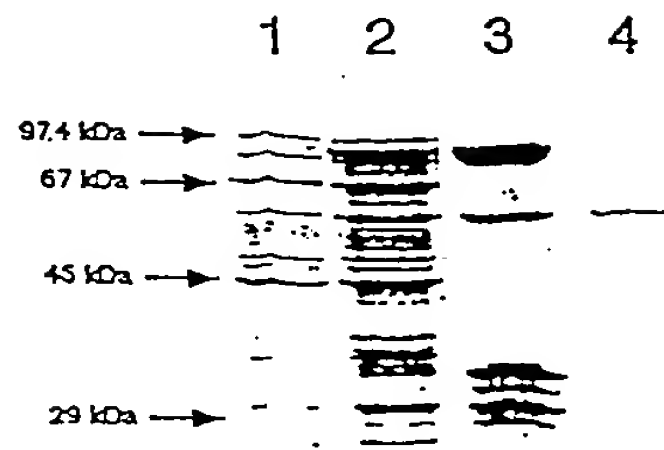
09573441.100901

FIGURE 9



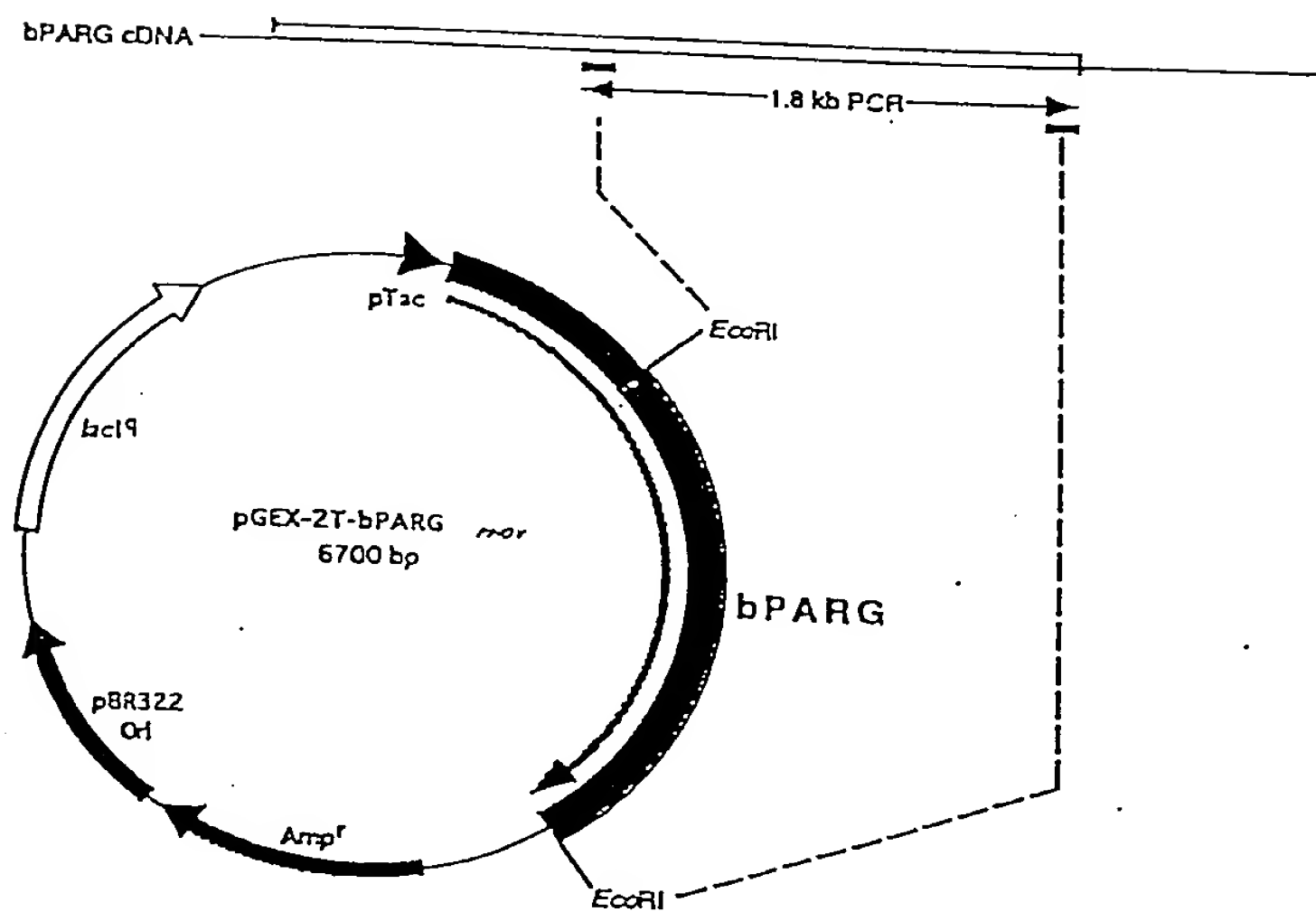
100000-100000

FIGURE 10



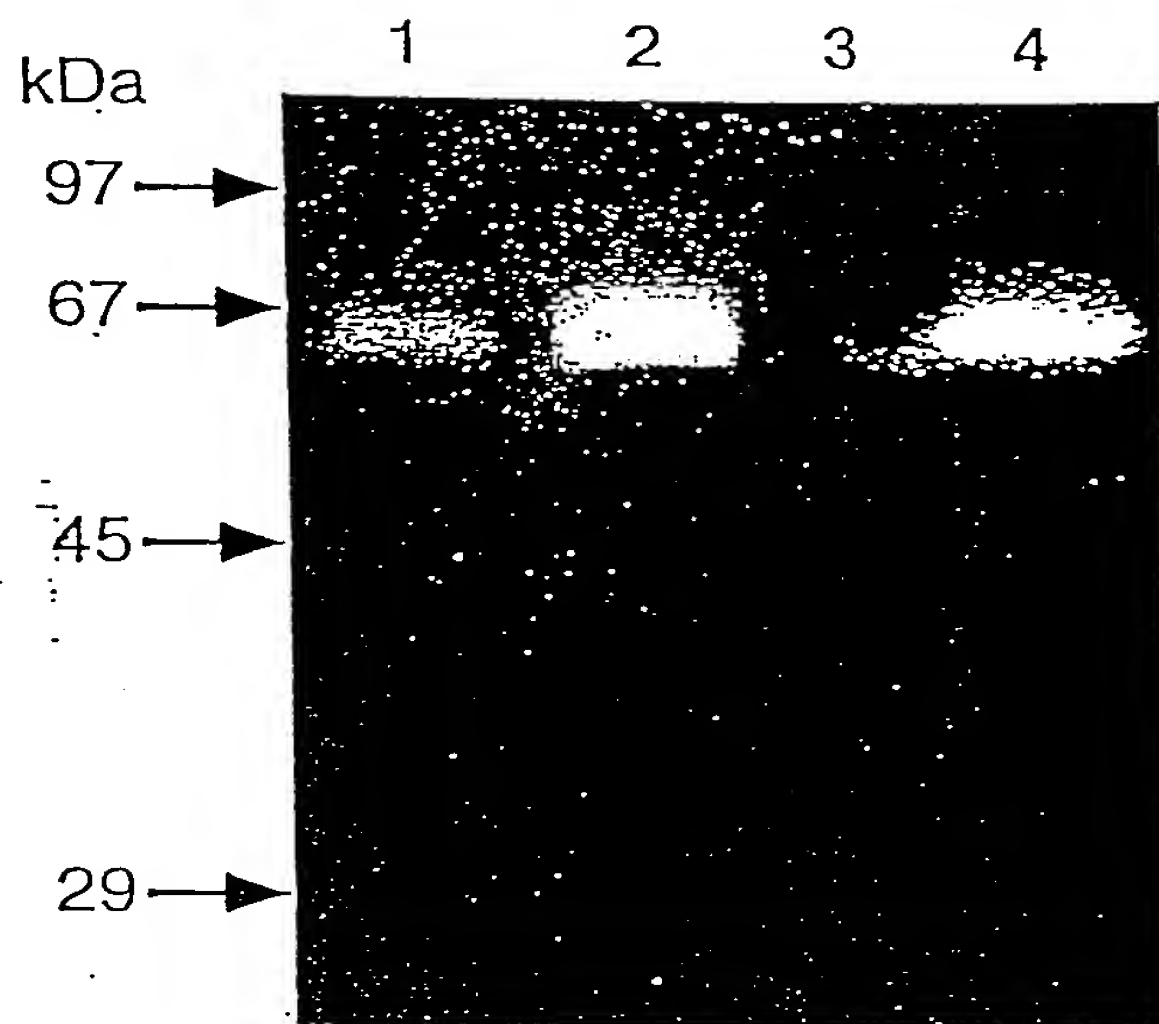
0907447-1000000

FIGURE 12



09573451-1005001

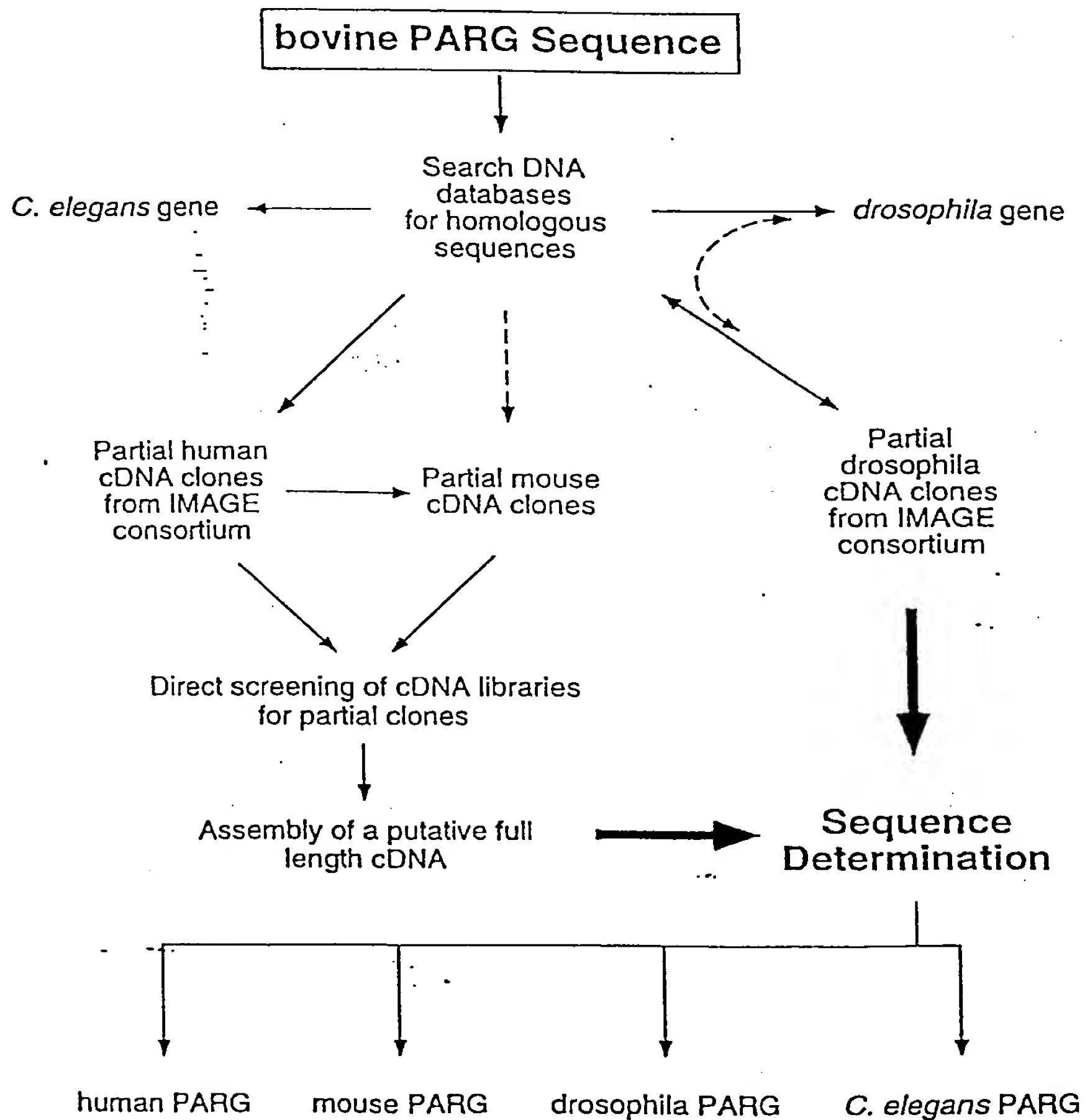
FIGURE 13



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FIGURE 14

Strategy to Obtain Homologous PARG Sequences



Domain Organization of PARs

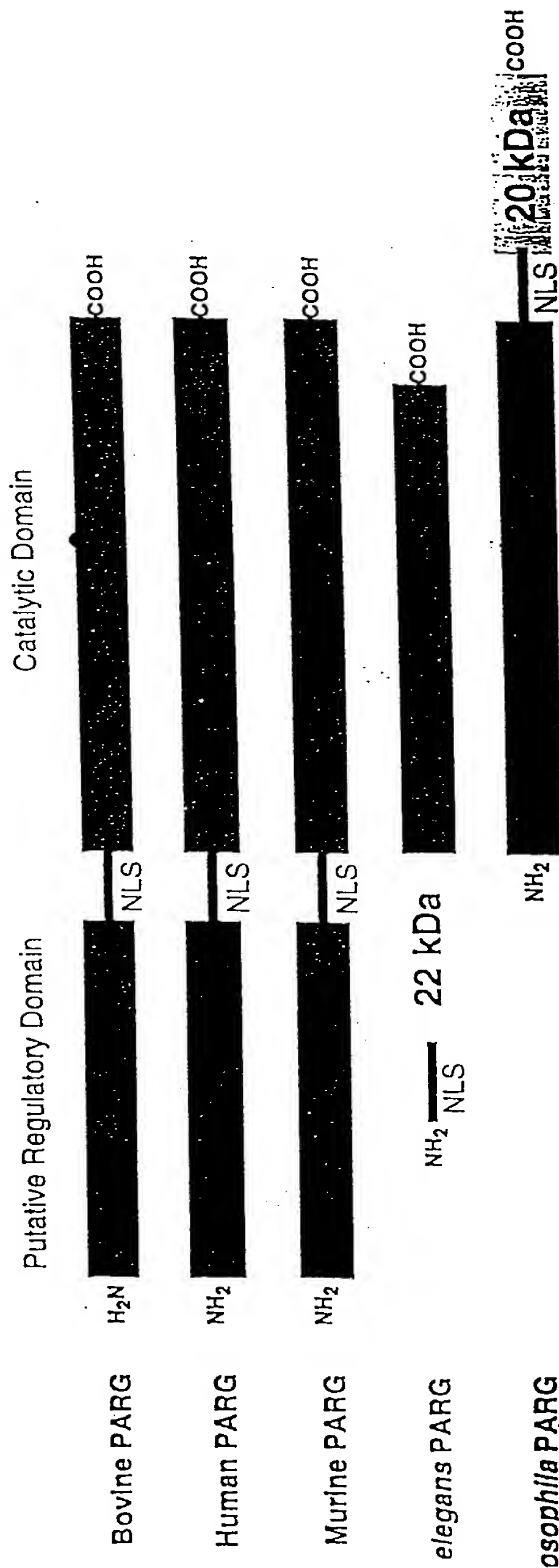


FIGURE 16

Multiple Alignment of Amino Acid Sequences of PARG from Different Species

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parg 1 MSAGPGCEPCTKRPRWDAAATSPFAASDARSFPGRQRRVLDSDAPVQFRVPPSSSQCALGRAGQHRGSATSLVFKQKTTISWMDTKGIKTVESESLSBK
parg 1 MNAGPGCEPCTKATRWGAATTS . PAASDARSFPGRQRRVLDPKDAEVQFRVPPSSPACVPGQAGQHRGSATSLVFKQKTTISWMDTKGIKTAESESLSBK
parg 1 MSAGPGWEPCTKA . RWGAAGTSAPTASDSRFPGRQRRVLDPKDAEVQFRVPPSSPACVSGRAGPHRGNATSFVFKQKTTITWMDTKGPKTAESE . . . BK
parg 1 -----
parg 1 -----

parg 101 EENNTRREESMMSSVQKDNFYQHNMKEKLENVSQLGFDKSPVEKGTQYLKQEQTAAAMCKWQNEGPHSERLLESEPPAVTLVPEQFSNANVDQSSPKDDDESDT
parg 100 EENNTRIESMMSSVQKDNFYQHNVKLVHVSQSLDKSLTEKSTQYLNQHQTAAAMCKWQNEGKHEQLLESEPPQTVTLVPEQFSNANIDRSPQNDDESDT
parg 97 EENNTRIDSMSSVQKDNFYPHKVKLENVSQLNLDKSPTEKSSQYLNQQQTASVCKWQNEGKHAQQLLASEPPACTPLPKQLSNANICQSPRTDDDESDT
parg 1 -----
parg 1 -----MSKKFIELGDPVTQDEKDYEDI

parg 201 NSBESRDNQQLFTHVKL . . . ANAKQTMEDQGRREARSHQKCGKACHPAEACAGCQQRRETDVVSSEPLSDTGSSEVGTGLKNAHRLNRQESSLGNSPPFEEK
parg 200 DSEHNRDNQQLFTTVKL . . . ANAKQTTEDHAREBAKSHQKCSKCEPGEDEASCQQRRETDVVPKSPPLSDVGSSEVGTGSKHNDKLIQESCLGNSPPFEEK
parg 197 DHEEDRDNQQLFTPIKL . . . ANTKPTVGDGQ . . . ARSNCKCSGSRQSVKDCGTGCQQRREVDVLPESPLSDVGAEDIGTGPKNHDKLTGQESSLGDSPPFEEK
parg 1 -----
parg 23 VGVGFAGVQPTMKRRRLTEHGNTTESKEDPEEPKSRDVFVSSQSSDESQEDSAENPEIAKEVSENCENLTETLKISNIESLDNVTERSEHTLDH . . . HK

parg 298 ESEFESPMVDVNSKNSCQDSEADEETSPOFDE . QEDSSSAQTANKPSRFQPREADTELKRSSAKGGEIRLHFQFEGGESRAGMN . DVNAKRPGSTSSLN
parg 297 ESEFESPMVDVNSKNSCQDSEADEETSPOFDE . QEDGSSSQTANKPSRFQARDADIEFRKRISTKGGEVRLHFQFEGGESRTGMN . DLNAKLPONISSLN
parg 291 ESEFESPMVDVNSKNSCQDSEADEETSPOFDE . QDDRSS . QTANKLSSCQAREADGDLRKRYLTGQSEVRLHFQFE . GENNAGTS . DLNAKPSGNSSSLN
parg 1 -----
parg 119 STEPMEE . DVNHRKSHIDVAINSDEDDDELVLLENKEMRDGEQVQQLS . . QDLFADDQELIEYPGIMKDTTITQDITDSEVETAQRMEMIRETEADSTFVG

parg 396 VECRNSKQHGKDKSKITDHFMRVPKAEKRRKEQCEMKHQRTERRKIPKIYPPHLSPDKKWLGTPIEEM . . RMPRCGIRLPPLRPSANHTVTIRVDLLRIG
parg 395 VECRNSKQHGKDKSKITDHLMLPKAEKRRKEQWETKQRTERKIPKIYPPHLSPDKKWLGTPIEEM . . RMPRCGIRLPPLRPSANHTVTIRVDLLRAG
parg 387 VECRNSKQHGKDKSKITDHFMRISKSEDRRKEQCEVRHQRTERRKIPKIYPPHLPPEKKWLGTPIEEM . . RMPRCGIHLPSLRPSASHTVTIRVDLLRAG
parg 32 . . . . . TNRLGK . . . ALCLNCARMSKSPDGGISEIE . . . . . TERE . PENLANSL . . . . . DDSWRGVSMEDIAHRNRQPFELNLPVVTAGNLHRVMIQLPIRET .
parg 216 EDSKATKTIVRTSSSSP . . . LSTVSTCEAPAKGRARMYQKELEKHVIAFTEGNLT . . . . . LQPDNLKVDPDNRNRYI . CTIPNFPASQG . . . KLRED . NRYG

parg 494 EVPK . PPFTEPKDLMDNKHVKMPCSEQNLYPVEDENGE . RAAGSRWELIQTALLNRLTRPQNLKDAILKYNVAYSKKNDFTALIDFWDKVLEBAEAQHLY
parg 493 EVPK . PPFTHYKDLMDNKHVKMPCSEQNLYPVEDENGE . RTAGSRWELIQTALLNKFTRPQNLKDAILKYNVAYSKKNDFTALIDFWDKVLEBAEAQHLY
parg 485 EVPK . PPFTEYKDLMDNKHVKMPCSEQNLYPVEDENGE . RTAGSRWELIQTALLNKFTRPQNLKDAILKYNVAYSKKNDFTALVDFWDKVLEBAEAQHLY
parg 115 . PPR . PIKSPGK . . . WDSEEVRLPCAPESKIPRENPDGS . TTIDFRNEMIERALLQPIKTCEELQAAIISYNTTYRDQWHFRALHQLLDEELDESETRVFP
parg 303 . . PKIVLPQRNRE . FDSRGR . . . RDSYFYFKRKL DGYLKCYKTTGTFMFVGLLH . . . . . NMWE . . FDPDITIK . . . . . LPAL . BMYIKEMSELVGRBEV

parg 592 QSILPDMVKIALCLPNICTQPIPLKQKMNHSITMSQEIQIASLLANAFCTFPRRNA . KMKSEYSSYPDINFNRLFEGRSSRKPEKLTFLFCYFRV . . T
parg 591 QSILPDMVKIALCLPNICTQPIPLKQKMNHSITMSQEIQIASLLANAFCTFPRRNA . KMKSEYSSYPDINFNRLFEGRSSRKPEKLTFLFCYFRV . . T
parg 583 QSILPDMVKIALCLPNICTQPIPLKQKMNHSITMSQEIQIASLLANAFCTFPRRNA . KMKSEYSSYPDINFNRLFEGRSSRKPEKLTFLFCYFRV . . T
parg 210 EDLLPRIIRLALRLPDLIQSPVPLKHEKKNASLSLQQQISCLLANAFCTFPRRNTLKRKSEYSTFPDINFNRLYQSTGPAVLKELKCMHYFRVVCPT
parg 384 LEKFARVARIAKTAEDILPERIYRLVGDVE . SATLSHKQCAALVARMFFA . . . . . RPDSPFS . . . . . FCRILSSDKSICVEKLFLLFTYF . . . . .

parg 689 EKK . . . . PTGLVTFTQSL . L . ED . F . PEWERCEKLL . . . . . TRLVHTIEGTIEGHGQGMQLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDE
parg 688 EKK . . . . PTGLVTFTQSL . L . ED . F . PEWERCEKPL . . . . . TRLVHTIEGTIEGHGQGMQLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIIISRLFTFVLDE
parg 680 EKK . . . . PTGLVTFTQSL . L . ED . F . PEWERCEKPL . . . . . TRLVHTIEGTIEGHGQGMQLQVDFANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDE
parg 310 ERDASNVPTGVVTFVRRSGLPFE . L . IDWSQSAAPLGDVPLHVDAGETIEDEGIGLLQVDFANKYLGGGVVLEGGCVQEEIRFVICPELLVGLFTECLRP
parg 463 DKMSMDPPDGAVSF . RLTKMDKDTFNEEW . KDKKLRLSLEVEVEFFDEMLIEDTAL . CTQVDFANEHLGGGVVLEGGSVQEEIRFLMCPMMVGMHLLCEKMKQ

parg 779 NECLIITGTEQYSEYTGIAETIRWA . . . . . RSEHEDRSE . RDDWQRRTEIIVADALHFR . RYLD . . . . . QFVPEKIRRELHKAICGFLRPGVSEENLSAVA
parg 778 NECLIITGTEQYSEYTGIAETIRNS . . . . . RSEEDGSE . RDDCERRCTEIVADALHFR . RYLD . . . . . QFVPEKMRRELHKAICGFLRPGVSEENLSAVA
parg 770 NECLIITGTEQYSEYTGIAETIRNA . . . . . RSEHEDGSE . RDDWQRRCTEIVADALHFR . RYLD . . . . . QFVPEKVRRELHKAICGFLRPGVSEENLSAVA
parg 408 FEALVHLGABRISNYTGIAETIRNS . . . . . GNFEEDSTP . RDSSGRROTAIVADALHFA . QSEH . . . . . QYREDLMERELHKAICGFLVEMHVTTP . . PGVA
parg 560 LEAISIVGAIYVFSYTGIGHTLKNABLQPNHESRQNTNEFRDRPGRRLRVETIAIDAILFKGSKLDCQTEQLNKANIIREMKKASIGFMSQGPFTNIP . IV

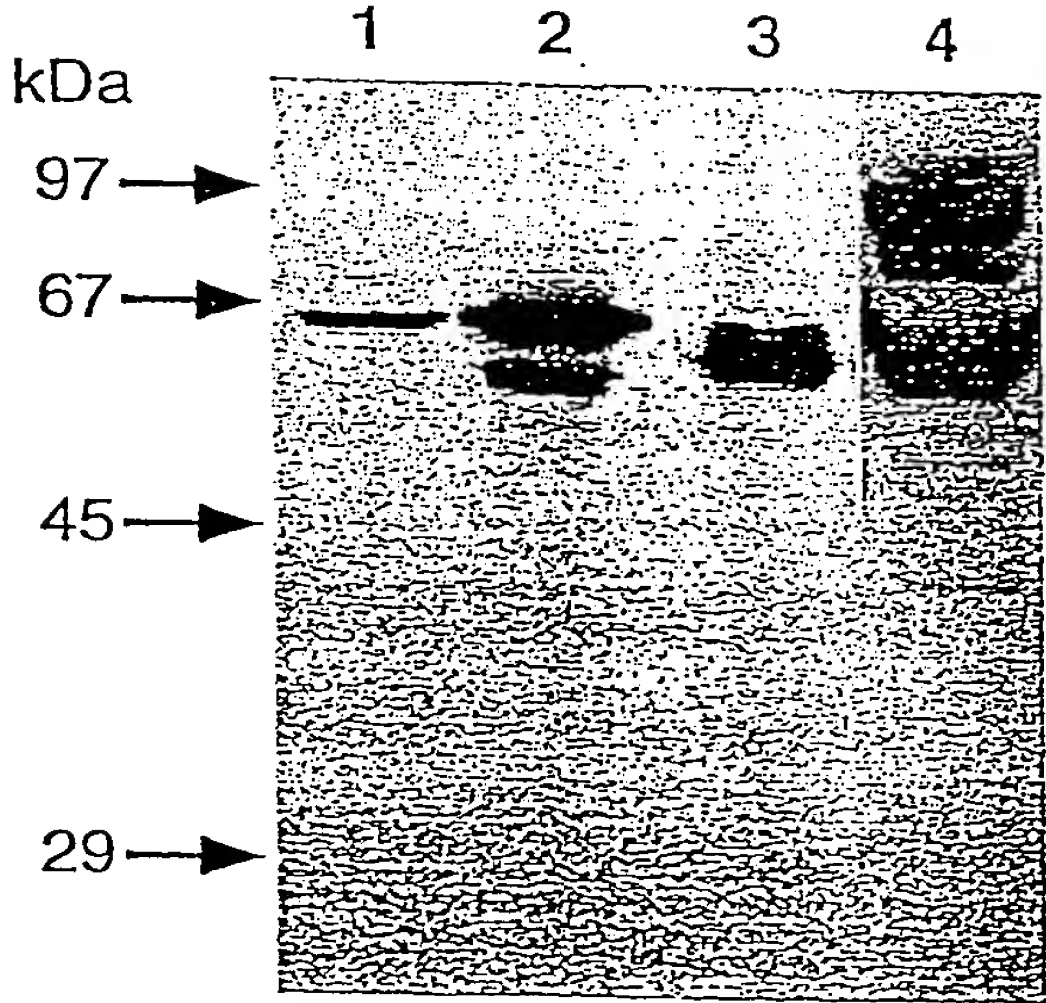
parg 868 TGNWCCGAFGGDARLKALIQILAAAVARDDVVIYFTFGDSELMRDIYSMTFLTERKLTGGE . VIKLLRLRYINEECRNCSTPGP . . . . . DIKLYPFIYHA
parg 867 TGNWCCGAFGGDARLKALIQILAAAAAERDDVVIYFTFGDSELMRDIYSMTFLTERKLTGGE . VIKLLRLRYINEECRNCSTPGP . . . . . DIKLYPFIYHA
parg 859 TGNWCCGAFGGDARLKALIQILAAAAAERDDVVIYFTFGDSELMRDIYSMTFLTERKLTGGE . VIKLLRLRYINEECRNCSTPGP . . . . . DIKLYPFIYHA
parg 495 TGNWCCGAFGGDSILKALLQLMVCAQLGRPLAITYTFGNVBFRRDDFHEMWLLFRNDGTTVQQ . LWS . ILRSYSRLIKEKSSKEPRENKASKKLLDPI . .
parg 659 TGNWCCGAFNGDKPLKFIIQVIAAGVADRPLEFCSPGEPELAACKKIIERMKQKQDVTLGKSCFSIFS . . . . .

parg 961 VESCTQTTNQPGQRTGA . . . . .
parg 960 VESCAETADHSGQRTGT . . . . .
parg 952 VESSAETTDMPGQKAGT . . . . .
parg 590 KEELKKVRDVPGEASABAGSSRVAGLGEGKSETSAKSSPELNKQPARPQITITQQSTDLLPAQLSQDNSNSEDQALLMLSDDEERANAMMEASLEAKS
parg 727 -----

parg 978 -----
parg 977 -----
parg 969 -----
parg 690 SVEISNSSTTSKTSSTATKSMGSGGRQLSLLEMLDTEYERKGSASKRPRKSPNCSKAEGSAKSARKEDVTDKDEKDDIVD
parg 727 -----

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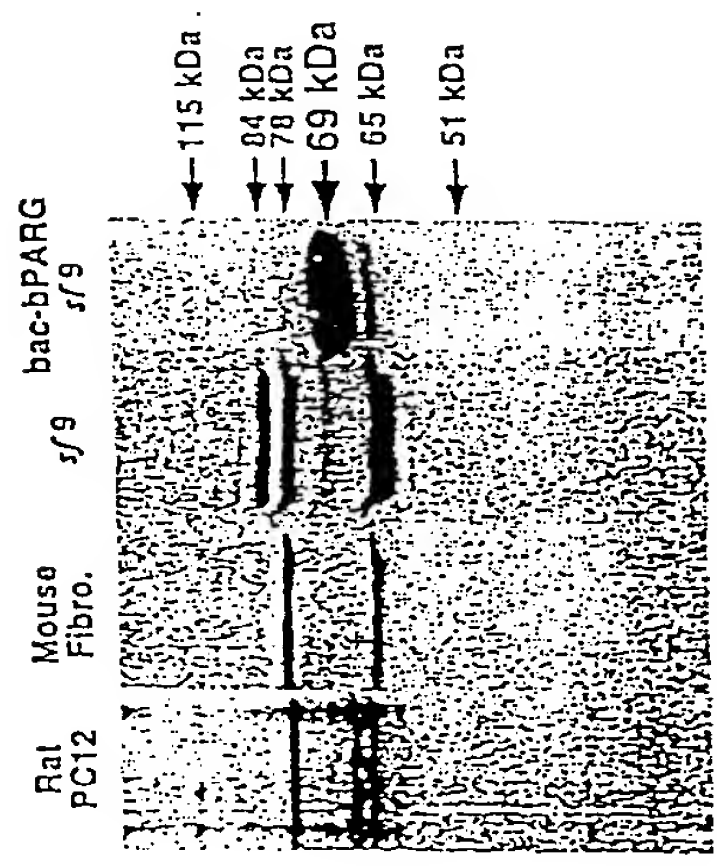

FIGURE 17



0997344.1009001

B

Cell Extracts



A

Bovine Tissue

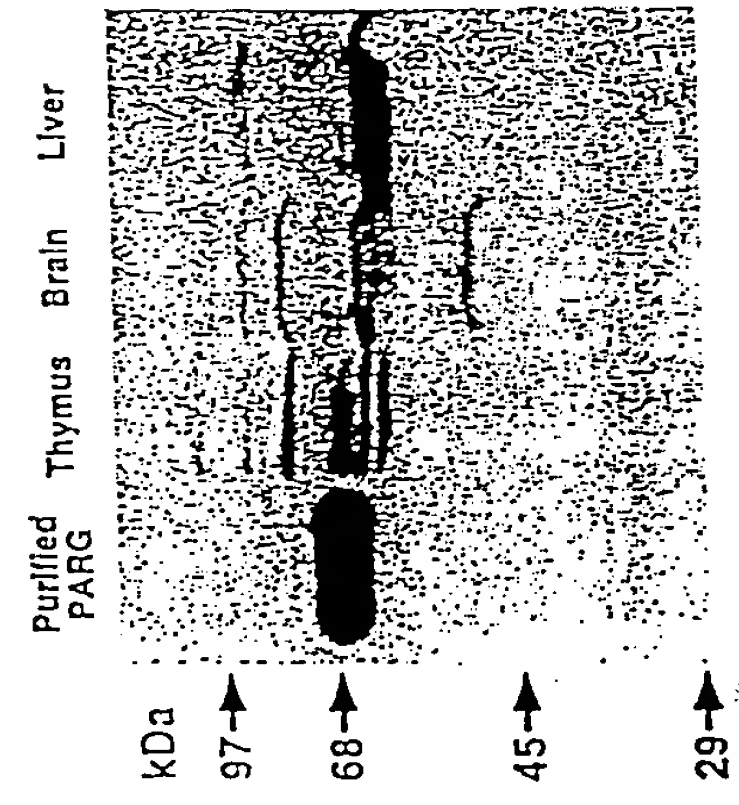


FIGURE 18

FIGURE 19

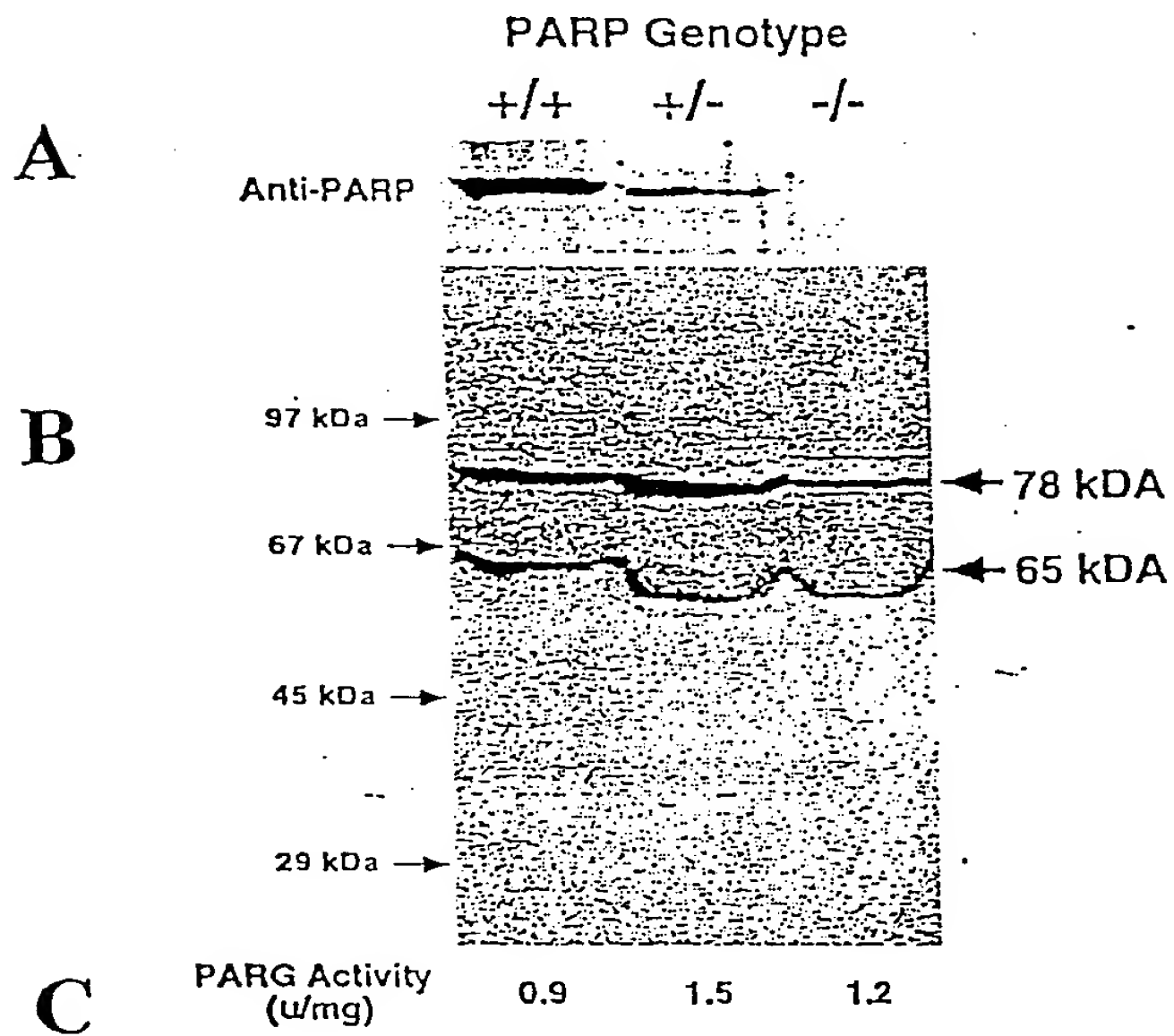


FIGURE 20

Genomic cloning of the PARC gene

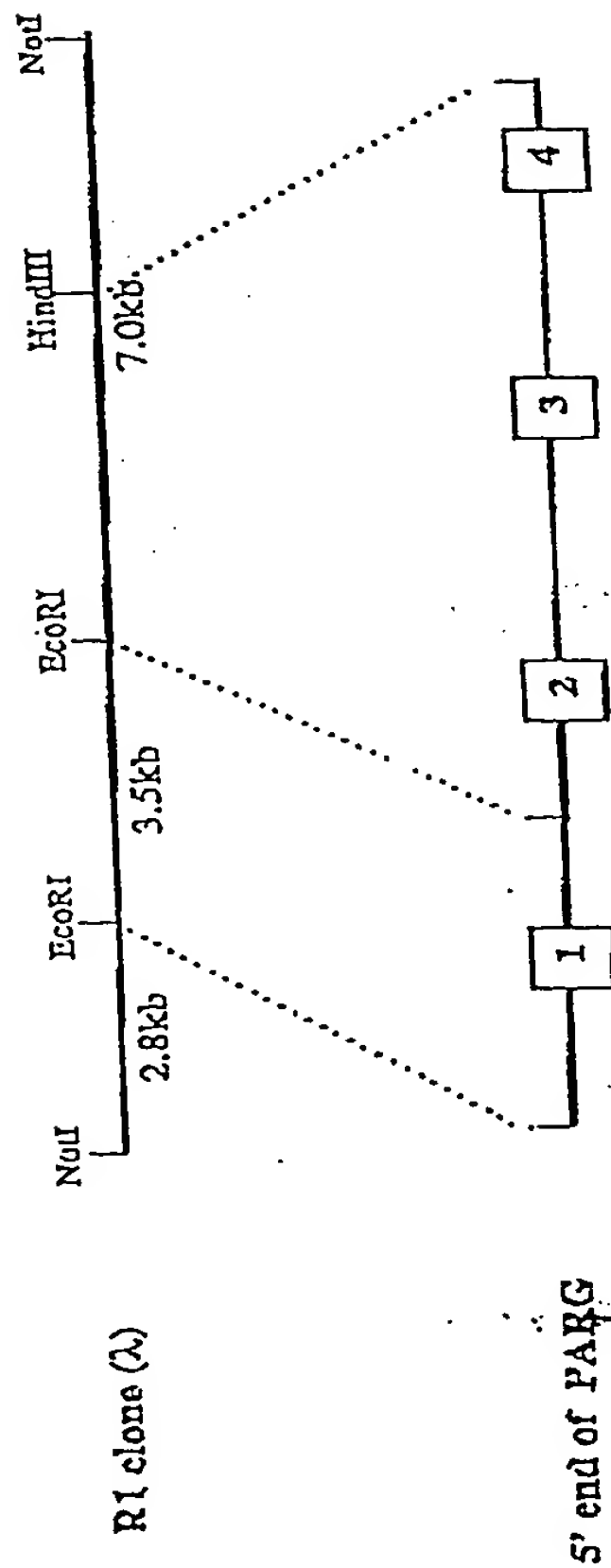


FIGURE 21
FIGURE 21

